

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 7, 2005, 12:16:15 ; Search time 12 seconds
(without alignments)
233.150 Million cell updates/sec

Title: US-09-285-531A-2
Perfect score: 2802
Sequence: 1 MAPVAVMAALAVGLELWAAA.....PSTSFLLPMGPSPARGSTG 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1421.5	50.7	461	7 US-11-132-285-6	Sequence 6, Appli
2	1421.5	50.7	461	7 US-11-182-946-4	Sequence 4, Appli
3	1302	46.5	235	7 US-11-126-126-16	Sequence 16, Appli
4	381	13.6	349	7 US-11-182-946-13	Sequence 13, Appli
5	373	13.3	355	7 US-11-182-946-14	Sequence 14, Appli
6	371	13.2	350	7 US-11-132-285-41	Sequence 41, Appli
7	347.5	12.4	595	7 US-11-182-946-9	Sequence 9, Appli
8	313.5	11.2	415	7 US-11-182-946-6	Sequence 6, Appli
9	302.5	10.8	277	7 US-11-182-946-10	Sequence 10, Appli
10	301.5	10.8	359	7 US-11-105-172-2	Sequence 2, Appli
11	301.5	10.8	391	7 US-11-105-172-4	Sequence 4, Appli
12	281.5	10.0	909	7 US-11-076-187-4	Sequence 4, Appli
13	241	8.6	211	7 US-11-132-839-12	Sequence 12, Appli
14	239	8.5	246	7 US-11-132-839-8	Sequence 8, Appli
15	238	8.5	195	7 US-11-132-839-11	Sequence 11, Appli
16	238	8.5	203	7 US-11-132-839-10	Sequence 10, Appli
17	216	7.7	669	7 US-11-076-187-3	Sequence 3, Appli
18	215.5	7.7	833	7 US-11-076-187-5	Sequence 5, Appli
19	212.5	7.6	160	7 US-11-132-839-7	Sequence 7, Appli
20	208	7.4	277	7 US-11-132-285-3	Sequence 3, Appli
21	208	7.4	277	7 US-11-182-946-12	Sequence 12, Appli
22	193	6.9	3717	6 US-10-821-234-1076	Sequence 1076, Ap
23	189.5	6.8	685	6 US-10-131-826A-88	Sequence 88, Appli
24	189.5	6.8	685	7 US-11-078-735-19	Sequence 19, Appli
25	189	6.7	427	7 US-11-182-946-5	Sequence 5, Appli

26	185	6.6	255	7 US-11-182-946-11	Sequence 11, Appli
27	180.5	6.4	455	7 US-11-182-946-3	Sequence 3, Appli
28	177	6.3	4419	6 US-10-821-234-1155	Sequence 1155, Ap
29	175	6.2	5179	7 US-11-108-172-1068	Sequence 1068, Ap
30	163.5	5.8	575	6 US-10-980-388-46	Sequence 46, Appli
31	162.5	5.8	259	6 US-10-131-826A-300	Sequence 300, Appli
32	162.5	5.8	259	7 US-11-182-946-2	Sequence 2, Appli
33	161	5.7	156	7 US-11-132-839-9	Sequence 9, Appli
34	161	5.7	161	7 US-11-126-126-2	Sequence 2, Appli
35	153.5	5.5	468	7 US-11-076-187-2	Sequence 2, Appli
36	151	5.4	334	6 US-10-514-057-6	Sequence 6, Appli
37	147.5	5.3	544	6 US-10-980-388-40	Sequence 40, Appli
38	147.5	5.3	1076	6 US-10-131-826A-219	Sequence 219, Appli
39	144.5	5.2	106	7 US-11-126-126-4	Sequence 4, Appli
40	144.5	5.2	106	7 US-11-126-126-8	Sequence 8, Appli
41	144.5	5.2	109	7 US-11-182-946-7	Sequence 7, Appli
42	141	5.0	335	7 US-11-182-946-7	Sequence 7, Appli
43	140	5.0	101	7 US-11-126-126-12	Sequence 12, Appli
44	140	5.0	1028	7 US-11-067-121-7	Sequence 7, Appli
45	140	5.0	1036	6 US-10-131-826A-142	Sequence 142, Appli

ALIGNMENTS

RESULT 1
US-11-132-285-6
; Sequence 6, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11PI
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-132-285-6

Query Match 50.7%; Score 1421.5; DB 7; Length 461;
Best Local Similarity 58.4%; Pred No. 1.7e-85;
Matches 301; Conservative 30; Mismatches 97; Indels 87; Gaps 12;

QY	1	MAPVAVMAALAVGLELWAAAALPAQVAFTPYAPFGSTCRLEYYDQTAQMCCSKCSPG	60
Db	1	MAPVAVMAALAVGLELWAAAALPAQVAFTPYAPFGSTCRLEYYDQTAQMCCSKCSPG	60
QY	61	QKAVFCTKTSDTVCDSCEDSTYTLQWVPECLSCGRCSDDQVETQACTREQNRITCTC	120
Db	61	QKAVFCTKTSDTVCDSCEDSTYTLQWVPECLSCGRCSDDQVETQACTREQNRITCTC	120
QY	121	RPGWYCALSKQEGCRCLCAPLRKCRPGFGVARPGTETSDVWCKPCAPGTFSTNTSSTDICR	180
Db	121	RPGWYCALSKQEGCRCLCAPLRKCRPGFGVARPGTETSDVWCKPCAPGTFSTNTSSTDICR	180

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OM protein - protein search, using sw model

Run on: December 7, 2005, 12:16:00 ; Search time 165 Seconds
(without alignment)
1268.682 Million cell updates/sec

Title: US-09-285-531A-2
Perfect score: 2802
Sequence: 1 MAPVAVMAALAVGLELWAAA.....PSTSFLLPMGPPPAEGSTG 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2674.5	95.4	720	4	US-10-363-427-8
2	2332	83.2	659	4	US-10-363-427-12
3	1429.5	51.0	566	5	US-10-677-877A-10
4	1427.5	50.9	461	3	US-09-800-909-2
5	1427.5	50.9	461	3	US-09-758-124-2
6	1427.5	50.9	461	3	US-09-800-908-3
7	1427.5	50.9	461	3	US-09-902-176A-50
8	1427.5	50.9	461	3	US-09-902-176A-52
9	1427.5	50.9	461	4	US-10-164-592-3
10	1427.5	50.9	461	4	US-10-252-408-2
11	1427.5	50.9	461	4	US-10-420-785-2
12	1427.5	50.9	461	4	US-10-423-927-2
13	1427.5	50.9	461	4	US-10-411-037-32
14	1427.5	50.9	461	4	US-10-411-026-32
15	1427.5	50.9	461	4	US-10-410-962-32
16	1427.5	50.9	461	4	US-10-411-049-32
17	1427.5	50.9	461	4	US-10-410-930-32
18	1427.5	50.9	461	4	US-10-410-997-32
19	1427.5	50.9	461	4	US-10-411-012-32
20	1427.5	50.9	461	4	US-10-287-994-32
21	1427.5	50.9	461	4	US-10-410-913-32
22	1427.5	50.9	461	4	US-10-632-929-3
23	1427.5	50.9	461	4	US-10-748-112-9
24	1427.5	50.9	461	5	US-10-370-715B-112
25	1427.5	50.9	461	5	US-10-410-980-32
26	1427.5	50.9	461	5	US-10-901-735-1
27	1427.5	50.9	461	5	US-10-775-180-152

28	1427.5	50.9	461	5	US-10-775-180-155
29	1427.5	50.9	461	5	US-10-410-897-32
30	1427.5	50.9	461	5	US-10-492-261-32
31	1427.5	50.9	461	5	US-10-775-204-462
32	1427.5	50.9	461	5	US-10-775-204-467
33	1427.5	50.9	461	6	US-11-019-829-112
34	1427.5	50.9	502	5	US-10-677-877A-12
35	1421.5	50.7	461	3	US-09-826-212-4
36	1421.5	50.7	461	3	US-09-896-096A-17
37	1421.5	50.7	461	3	US-09-894-924-17
38	1421.5	50.7	461	3	US-09-840-707A-17
39	1421.5	50.7	461	3	US-09-935-727-6
40	1421.5	50.7	461	3	US-09-902-176A-54
41	1421.5	50.7	461	4	US-10-046-433-6
42	1421.5	50.7	461	4	US-10-038-557A-17
43	1421.5	50.7	461	4	US-10-186-643-4
44	1421.5	50.7	461	4	US-10-418-242-6
45	1421.5	50.7	461	4	US-10-456-819-17

ALIGNMENTS

RESULT 1
US-10-363-427-8
; Sequence 8, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MeDexGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 8
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-8

Query Match	95.4%	Score 2674.5	DB 4	Length 720
Best Local Similarity	96.0%	Pred. No. 9.9e-149		
Matches 481	Conservative 1	Mismatches 4	Indels 15	Gaps 1
Qy	1	MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPPGSTCRLREYDYDTAQMCCSKCSPG	60	
Db	1	MAPVAVMAALAVGLELWAAAHALPAQVAFTPYAPPGSTCRLREYDYDTAQMCCSKCSPG	60	
Qy	61	QHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGSCSSDQVETQACTREQNRITC	120	
Db	61	QHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGSCSSDQVETQACTREQNRITC	120	
Qy	121	RPQWYCALSKOEGRCLCAPLRCRPGGVARPGTSTSDVVKPCAPGTFSTNTSDICR	180	
Db	121	RPQWYCALSKOEGRCLCAPLRCRPGGVARPGTSTSDVVKPCAPGTFSTNTSDICR	180	
Qy	181	PHQICNVVAIPGNASMDAVCTSTPSTRMAPAGVHLPPQVSTRQHTQPTPEPSTAPSTS	240	
Db	181	PHQICNVVAIPGNASMDAVCTSTPSTRMAPAGVHLPPQVSTRQHTQPTPEPSTAPSTS	240	
Qy	241	FLPMPGPPPARGGGGGGGGSDPAQVAFTPYAPPGSTCRLREYDYDTAQMCCS	300	
Db	241	FLPMPGPPPARGGGGGGGGSDPAQVAFTPYAPPGSTCRLREYDYDTAQMCCS	285	
Qy	301	KCSPGOHAKVCTKTSDTVCDSCESTYTLNWNVPECLSCGSCSSDQVETQACTREQNR	360	

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OM protein - protein search, using sw model

Run on: December 7, 2005, 12:10:29 ; Search time 26 Seconds
(without alignments)
1593.097 Million cell updates/sec

Title: US-09-285-531A-2
Perfect score: 2802
Sequence: 1 MAPVAVMAALVGLLEWAA.....PSTSLPMGSPPAEGSTG 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1427.5	50.9	461	1	US-08-385-229-2
2	1427.5	50.9	461	1	US-08-650-000-2
3	1427.5	50.9	461	2	US-08-477-347-3
4	1427.5	50.9	461	2	US-08-476-862-2
5	1427.5	50.9	461	2	US-08-406-824A-2
6	1427.5	50.9	461	2	US-09-800-909-2
7	1427.5	50.9	461	2	US-09-758-124-2
8	1427.5	50.9	461	2	US-09-800-908-3
9	1427.5	50.9	461	2	US-09-949-016-6019
10	1427.5	50.9	461	6	5395760-2
11	1427.5	50.9	491	2	US-09-949-016-7840
12	1421.5	50.7	461	2	US-09-042-785A-7
13	1421.5	50.7	461	2	US-09-006-333A-4
14	1421.5	50.7	461	2	US-09-573-986-4
15	1421.5	50.7	461	2	US-09-896-096A-17
16	1421.5	50.7	461	2	US-10-046-433-6
17	1409	50.3	257	2	US-09-579-845-10
18	1409	50.3	518	1	US-08-385-229-4
19	1409	50.3	518	2	US-09-573-845-1
20	1409	50.3	518	2	US-09-579-845-3
21	1402	50.0	486	1	US-08-243-010-1
22	1308.5	46.7	439	2	US-10-360-101-226
23	1308	46.7	235	2	US-09-580-235-8
24	1308	46.7	235	2	US-09-580-181-8
25	1308	46.7	235	2	US-09-102-530-8
26	1305	46.6	235	2	US-09-580-235-2
27	1305	46.6	235	2	US-09-580-235-4

28	1305	46.6	235	2	US-09-580-181-2	Sequence 2, Appli
29	1305	46.6	235	2	US-09-580-181-4	Sequence 4, Appli
30	1305	46.6	235	2	US-09-102-530-2	Sequence 2, Appli
31	1305	46.6	235	2	US-09-102-530-4	Sequence 4, Appli
32	1302	46.5	235	2	US-09-326-394-4	Sequence 4, Appli
33	1302	46.5	235	2	US-09-580-235-6	Sequence 6, Appli
34	1302	46.5	235	2	US-09-580-181-6	Sequence 6, Appli
35	1302	46.5	235	2	US-09-102-530-6	Sequence 6, Appli
36	1263	45.1	227	2	US-08-974-022-48	Sequence 48, Appl
37	1263	45.1	227	2	US-08-795-445A-48	Sequence 48, Appl
38	1263	45.1	227	2	US-08-795-447A-48	Sequence 48, Appl
39	1263	45.1	227	2	US-08-974-186-48	Sequence 48, Appl
40	1263	45.1	227	2	US-08-795-446B-48	Sequence 48, Appl
41	1263	45.1	227	2	US-08-706-945D-134	Sequence 134, App
42	1263	45.1	227	2	US-08-577-788C-48	Sequence 48, Appl
43	1068	38.1	189	2	US-09-422-680A-25	Sequence 25, Appl
44	935	33.4	163	2	US-09-523-323-54	Sequence 54, Appl
45	931	33.2	163	1	US-08-219-237B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-385-229-2
; Sequence 2, Application US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-385-229-2

Query Match 50.9%; Score 1427.5; DB 1; Length 461;
Best Local Similarity 58.6%; Pred. No. 33e-94;
Matches 302; Conservative 30; Mismatches 96; Indels 87; Gaps 12;
Qy 1 MAPVAVMAALVGLLEWAAHALPAQVAFYPAEPGTCRLREYDQTAQMCCSKSPG 60
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